SEQUENCE LISTING

<110> MOLONEY, MAURICE M.
DALMIA, BIPIN K.

<120> PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE PROTEINS ON OIL BODIES

<130> 034547/0106

<140> 09/897,425
<141> 2001-07-03

<150> 09/210,843
<151> 1998-12-18

<150> 08/846,021
<151> 1997-04-25

<150> 08/366,783
<151> 1994-12-30

<150> 08/142,418
<151> 1993-11-16

<150> 07/659,835
<151> 1991-02-22

<160> 55

<170> PatentIn Ver. 2.1

<210> 1
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actccccaga aacaaccggc gccaaattgc cggaattgct gacctgaaga cggaacatca 120

tcgtcgggtc cttgggcgat tgcggcggaa gatgggtcag cttgggcttg aggacgagac 180

ccgaatcgag tctgttgaaa ggttgttcat tgggatttgt atacggagat tggtcgtcga 240

gaggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggctttagag 300

agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg 360

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acctgcatta tcaaagcagt gacgtggtga aatttggaac ttttaagagg cagatagatt 420

tattatttgt atccattttc ttcattgttc tagaatgtcg cggaacaaat tttaaaacta 480

aatcctaaat ttttctaatt ttgttgccaa tagtggatat gtgggccgta tagaaggaat 540

ctattgaagg cccaaaccca tactgacgag cccaaaggtt cgttttgcgt tttatgtttc 600

ggttcgatgc caacgccaca ttctgagcta ggcaaaaaac aaacgtgtct ttgaatagac 660

tcctctcgtt aacacatgca gcggctgcat ggtgacgcca ttaacacgtg gcctacaatt 720

gcatgatgtc tccattgaca cgtgacttct cgtctccttt cttaatatat ctaacaaaca 780

ctcctacctc ttccaaaata tatacacatc tttttgatca atctctcatt caaaatctca 840

ttctctctag taaacaagaa caaaaaa atg gcg gat aca gct aga gga acc cat 894
                            Met Ala Asp Thr Ala Arg Gly Thr His
                              1               5

cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga   942
His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg
 10                  15                  20                  25

gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg   990
Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg
                 30                  35                  40

cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt   1038
Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu
             45                  50                  55

gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt   1086
Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val
         60                  65                  70

gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc   1134
Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu
     75                  80                  85

atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt   1182
Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe
 90                  95                  100                 105

ggc att gcc gct ata acc gtt ttc tct tgg att tac aag taagcacaca    1231
Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr Lys
                110                 115

tttatcatct tacttcataa ttttgtgcaa tatgtgcatg catgtgttga gccagtagct 1291

ttggatcaat ttttttggtc gaataacaaa tgtaacaata agaaattgca aattctaggg 1351

aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat 1411

catctatata ggtaaaatgc ttggtatgat acctattgat tgtgaatagg tac gca    1467
                                                    Tyr Ala
                                                        120
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acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg   1515
Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met
                125                 130                 135

aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac   1563
Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr
            140                 145                 150

gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt ggt   1611
Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg Gly
        155                 160                 165

ggc cag cac act act taagttaccc cactgatgtc atcgtcatag tccaataact   1666
Gly Gln His Thr Thr
    170

ccaatgtcgg ggagttagtt tatgaggaat aaagtgttta gaatttgatc aggggagat 1726

aataaaagcc gagtttgaat ctttttgtta taagtaatgt ttatgtgtgt ttctatatgt 1786

tgtcaaatgg tacc                                                  1800
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<211> 118
<212> PRT
<213> Arabidopsis thaliana

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Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
             20                  25                  30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
         35                  40                  45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
     50                  55                  60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
 65                  70                  75                  80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
                 85                  90                  95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
            100                 105                 110

Phe Ser Trp Ile Tyr Lys
        115
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<210> 3
<211> 55
<212> PRT
<213> Arabidopsis thaliana

<400> 3
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr
50 55

<210> 4
<211> 564
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(561)

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Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln
1 5 10 15

tat ccc cga gac cga gac cag tat tct atg atc ggt cga gac cgt gac 96
Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
20 25 30

cag tac tct atg atg ggc cga gac cga gac cag tac aac atg tat ggt 144
Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
35 40 45

cga gac tac tcc aag tct aga cag att gct aag gct gtt acc gca gtc 192
Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
50 55 60

acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc ctt gtt ggt 240
Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
65 70 75 80

act gtc att gct ttg act gtt gcc act cca ctc ctc gtt atc ttt agc 288
Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
85 90 95

cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc atc act ggc 336
Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
100 105 110

ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc gtc ttc tcc 384
Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
115 120 125

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tgg atc tat aag tac gca acg gga gag cac cca cag ggg tca gat aag   432
Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
    130                 135                 140

ttg gac agt gca agg atg aag ctg gga acc aaa gct cag gat att aaa   480
Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
145                 150                 155                 160

gac aga gct caa tac tac gga cag caa cat aca ggt ggt gag cat gac   528
Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
                165                 170                 175

cgt gac cgt act cgt ggt ggc cag cac act act taa                   564
Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
            180                 185
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<210> 5
<211> 187
<212> PRT
<213> Brassica napus

<400> 5

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Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln
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Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
            20                  25                  30

Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
        35                  40                  45

Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
    50                  55                  60

Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
65                  70                  75                  80

Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
                85                  90                  95

Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
            100                 105                 110

Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
        115                 120                 125

Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
    130                 135                 140

Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
145                 150                 155                 160

Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
                165                 170                 175

Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
            180                 185
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<210> 6
<211> 2733
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of pSBSOTPTNT containing the oleosin-chymosin fusion gene

<220>
<221> CDS
<222> (850)..(1203)

<220>
<221> CDS
<222> (1444)..(2724)

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gcgccaaatt gccggaattg ctgacctgaa gacggaacat catcgtcggg tccttgggcg 120

attgcggcgg aagatgggtc agcttgggct tgaggacgag acccgaatcg agtctgttga 180

aaggttgttc attgggattt gtatacggag attggtcgtc gagaggtttg agggaaagga 240

caaatgggtt tggctctgga gaaagagagt gcggctttag agagagaatt gagaggttta 300

gagagagatg cggcggcgat gacgggagga gagacgacga ggacctgcat tatcaaagca 360

gtgacgtggt gaaatttgga acttttaaga ggcagataga tttattattt gtatccattt 420

tcttcattgt tctagaatgt cgcggaacaa attttaaaac taaatcctaa atttttctaa 480

ttttgttgcc aatagtggat atgtgggccg tatagaagga atctattgaa ggcccaaacc 540

catactgacg agcccaaagg ttcgttttgc gttttatgtt tcggttcgat gccaacgcca 600

cattctgagc taggcaaaaa acaaacgtgt ctttgaatag actcctctcg ttaacacatg 660

cagcggctgc atggtgacgc cattaacacg tggcctacaa ttgcatgatg tctccattga 720

cacgtgactt ctcgtctcct ttcttaatat atctaacaaa cactcctacc tcttccaaaa 780

tatatacaca tctttttgat caatctctca ttcaaaatct cattctctct agtaaacaag 840

aacaaaaaa atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc 891
Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly
1 5 10

aga gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg 939
Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
15 20 25 30

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tcc gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct   987
Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala
                35                  40                  45

gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt   1035
Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu
            50                  55                  60

acc ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc   1083
Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu
        65                  70                  75

gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc   1131
Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu
    80                  85                  90

ctc atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata   1179
Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile
 95                 100                 105                 110

acc gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa  1233
Thr Val Phe Ser Trp Ile Tyr Lys
                115

ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc 1293

gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata 1353

cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc 1413

ttggtatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag  1467
                                Tyr Ala Thr Gly Glu His Pro Gln
                                    120                 125

gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct   1515
Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala
            130                 135                 140

cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt   1563
Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly
        145                 150                 155

ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act ctc   1611
Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu
    160                 165                 170

gtt cca cga gga tcc atg gct gag atc acc agg atc cct ctg tac aaa   1659
Val Pro Arg Gly Ser Met Ala Glu Ile Thr Arg Ile Pro Leu Tyr Lys
175                 180                 185                 190

ggc aag tct ctg agg aag gcg ctg aag gag cat ggg ctt ctg gag gac   1707
Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu Glu Asp
                195                 200                 205

ttc ctg cag aaa cag cag tat ggc atc agc agc aag tac tcc ggc ttc   1755
Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser Gly Phe
            210                 215                 220
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ggg gag gtg gcc agc gtg ccc ctg acc aac tac ctg gat agt cag tac   1803
Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr
        225                 230                 235

ttt ggg aag atc tac ctc ggg acc ccg ccc cag gag ttc acc gtg ctg   1851
Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu
    240                 245                 250

ttt gac act ggc tcc tct gac ttc tgg gta ccc tct atc tac tgc aag   1899
Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys
255                 260                 265                 270

agc aat gcc tgc aaa aac cac cag cgc ttc gac ccg aga aag tcg tcc   1947
Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser
                275                 280                 285

acc ttc cag aac ctg ggc aag ccc ctg tct atc cac tac ggg aca ggc   1995
Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly
            290                 295                 300

agc atg cag ggc atc ctg ggc tat gac acc gtc act gtc tcc aac att   2043
Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile
        305                 310                 315

gtg gac atc cag cag aca gta ggc ctg agc acc cag gag ccc ggg gac   2091
Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp
    320                 325                 330

gtc ttc acc tat gcc gaa ttc gac ggg atc ctg ggg atg gcc tac ccc   2139
Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro
335                 340                 345                 350

tcg ctc gcc tca gag tac tcg ata ccc gtg ttt gac aac atg atg aac   2187
Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn
                355                 360                 365

agg cac ctg gtg gcc caa gac ctg ttc tcg gtt tac atg gac agg aat   2235
Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn
            370                 375                 380

ggc cag gag agc atg ctc acg ctg ggg gcc atc gac ccg tcc tac tac   2283
Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr
        385                 390                 395

aca ggg tcc ctg cac tgg gtg ccc gtg aca gtg cag cag tac tgg cag   2331
Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln
    400                 405                 410

ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtg gcc tgt gag   2379
Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu
415                 420                 425                 430

ggt ggc tgt cag gcc atc ttg gac acg ggc acc tcc aag ctg gtc ggg   2427
Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly
                435                 440                 445
```

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ccc agc agc gac atc ctc aac atc cag cag gcc att gga gcc aca cag   2475
Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
            450                 455                 460

aac cag tac ggt gag ttt gac atc gac tgc gac aac ctg agc tac atg   2523
Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
        465                 470                 475

ccc act gtg gtc ttt gag atc aat ggc aaa atg tac cca ctg acc ccc   2571
Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
    480                 485                 490

tcc gcc tat acc agc caa gac cag ggc ttc tgt acc agt ggc ttc cag   2619
Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
495                 500                 505                 510

agt gaa aat cat tcc cag aaa tgg atc ctg ggg gat gtt ttc atc cga   2667
Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
                515                 520                 525

gag tat tac agc gtc ttt gac agg gcc aac aac ctc gtg ggg ctg gcc   2715
Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
            530                 535                 540

aaa gcc atc tgaaagctt                                            2733
Lys Ala Ile
        545
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<210> 7
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of pSBSOTPTNT containing the oleosin-chymosin fusion gene

<400> 7

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Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
  1               5                  10                  15

Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
            20                  25                  30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
        35                  40                  45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
    50                  55                  60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65                  70                  75                  80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
                85                  90                  95
```

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
100 105 110

Phe Ser Trp Ile Tyr Lys
115

<210> 8
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of pSBSOTPTNT containing the oleosin-chymosin fusion gene

<400> 8
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Ala Glu
50 55 60

Ile Thr Arg Ile Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu
65 70 75 80

Lys Glu His Gly Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly
85 90 95

Ile Ser Ser Lys Tyr Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu
100 105 110

Thr Asn Tyr Leu Asp Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr
115 120 125

Pro Pro Gln Glu Phe Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe
130 135 140

Trp Val Pro Ser Ile Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln
145 150 155 160

Arg Phe Asp Pro Arg Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro
165 170 175

Leu Ser Ile His Tyr Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr
180 185 190

Asp Thr Val Thr Val Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly
195 200 205

```
Leu Ser Thr Gln Glu Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp
    210                 215                 220

Gly Ile Leu Gly Met Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile
225                 230                 235                 240

Pro Val Phe Asp Asn Met Met Asn Arg His Leu Val Ala Gln Asp Leu
                245                 250                 255

Phe Ser Val Tyr Met Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu
            260                 265                 270

Gly Ala Ile Asp Pro Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro
        275                 280                 285

Val Thr Val Gln Gln Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile
    290                 295                 300

Ser Gly Val Val Val Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp
305                 310                 315                 320

Thr Gly Thr Ser Lys Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile
                325                 330                 335

Gln Gln Ala Ile Gly Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile
            340                 345                 350

Asp Cys Asp Asn Leu Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn
        355                 360                 365

Gly Lys Met Tyr Pro Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln
    370                 375                 380

Gly Phe Cys Thr Ser Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp
385                 390                 395                 400

Ile Leu Gly Asp Val Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg
                405                 410                 415

Ala Asn Asn Leu Val Gly Leu Ala Lys Ala Ile
            420                 425
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<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 9
Leu Val Pro Arg Gly
1   5

<210> 10
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 10
Phe Glu Gly Arg
1

<210> 11
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 11
Pro Leu Gly Pro
1

<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 12
Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 13
<211> 14
<212> DNA
<213> Daucus carota

<400> 13
acggtaacaa ctct 14

<210> 14
<211> 14
<212> DNA
<213> Zea mays

<400> 14
gcggtaacga cggc 14

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
cactgcagga actctctggt aa 22

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ctacccggga tcctgtttac tagagagaat g 31

<210> 17
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
aatcccatgg atcctcgtgg aacgagagta gtgtgctggc caccacgagt acggtcacgg 60
tc 62

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
cactgcagga actctctggt aagc 24

<210> 19
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19
gaggatccat ggtacgtcct gtagaaacc 29

<210> 20
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gtaaaacgac ggccagt 17

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oleosin/GUS fusion protein

<400> 21
Leu Val Pro Arg Gly Ser
1 5

<210> 22
<211> 9
<212> PRT
<213> Homo sapiens

<400> 22
Val Gln Gly Glu Glu Ser Asn Asp Lys
1 5

<210> 23
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
cgcggtacca tggctatacc caacctcg 28

<210> 24
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
cgcatcgatg ttcttgttta ctagagag 28

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gccatcgatc atatgttacg tcctgtagaa acccca 36

<210> 26
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
cgcggatcct cttccttcga tttgtttgcc tccctgc 37

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
cgcggatcca tggcggatac agctaga 27

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
tgctctagac gatgacatca gtggggtaac ttaagt 36

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic spacer sequence

<400> 29
Leu Val Pro Arg Gly Ser
1 5

<210> 30
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
atctctagaa ttcaactact cttgctcaaa g 31

<210> 31
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
gggttgctcg agatttctaa tcaatttat 29

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
taccatggct tcggaagaag ga 22

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
gaaagcttaa gccaagtgtt tg 22

<210> 34
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
ggccagcaca ctaccatgaa tggtctcgaa actcac 36

<210> 35
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ttaagcttca atcactctta ccttgctg 28

<210> 36
<211> 1002
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Published NADPH thioredoxin reductase sequence

<220>
<221> CDS
<222> (1)..(999)

<400> 36

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Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser	
1				5				10					15			
ggc	cca	gcg	gca	cac	acg	gcg	gcg	att	tac	gca	gct	agg	gct	gaa	ctt	96
Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu	
			20					25					30			
aaa	cct	ctt	ctc	ttc	gaa	gga	tgg	atg	gct	aac	gac	atc	gct	ccc	ggt	144
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly	
		35					40					45				
ggt	caa	cta	aca	acc	acc	acc	gac	gtc	gag	aat	ttc	ccc	gga	ttt	cca	192
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	
	50					55					60					

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gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg   240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65                  70                  75                  80

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat   288
Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
                85                  90                  95

ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc   336
Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
            100                 105                 110

gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc   384
Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
        115                 120                 125

ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc   432
Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
    130                 135                 140

tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa   480
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145                 150                 155                 160

cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac   528
Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
                165                 170                 175

ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat   576
Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
            180                 185                 190

gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct   624
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
        195                 200                 205

aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat   672
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
    210                 215                 220

gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc   720
Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225                 230                 235                 240

gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt   768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
                245                 250                 255

cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg   816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
            260                 265                 270

gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc   864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
        275                 280                 285
```

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gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc    912
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
    290                 295                 300

atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat    960
Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305                 310                 315                 320

tac tta caa gag att gga tct cag caa ggt aag agt gat tga            1002
Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
                325                 330
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<210> 37
<211> 1002
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (1)..(999)

<400> 37

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atg aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt     48
Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
  1               5                  10                  15

ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt     96
Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
            20                  25                  30

aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt    144
Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
        35                  40                  45

ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca    192
Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
    50                  55                  60

gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg    240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65                  70                  75                  80

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat    288
Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
                85                  90                  95

ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc    336
Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
            100                 105                 110

gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc    384
Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
        115                 120                 125

ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc    432
Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
    130                 135                 140
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tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa   480
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145                 150                 155                 160

cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac   528
Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
                165                 170                 175

ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat   576
Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
            180                 185                 190

gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct   624
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
        195                 200                 205

aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat   672
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
    210                 215                 220

gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc   720
Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225                 230                 235                 240

gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt   768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
                245                 250                 255

cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg   816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
            260                 265                 270

gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc   864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
        275                 280                 285

gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc   912
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
    290                 295                 300

atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat   960
Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305                 310                 315                 320

tac tta caa gag att gga tct cag caa ggt aag agt gat tga          1002
Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
                325                 330
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<210> 38
<211> 333
<212> PRT
<213> Arabidopsis sp.

<400> 38

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Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
  1               5                  10                  15
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Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
                20                  25                  30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
            35                  40                  45

Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
        50                  55                  60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65                  70                  75                  80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
                85                  90                  95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
            100                 105                 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
        115                 120                 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
    130                 135                 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145                 150                 155                 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
                165                 170                 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
            180                 185                 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
        195                 200                 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
    210                 215                 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225                 230                 235                 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
                245                 250                 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
            260                 265                 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
        275                 280                 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
    290                 295                 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305                 310                 315                 320
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Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
325 330

<210> 39
<211> 333
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Published NADPH thioredoxin reductase sequence

<400> 39
Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
1 5 10 15

Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
35 40 45

Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145 150 155 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 230 235 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
245 250 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
290 295 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305 310 315 320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
325 330

<210> 40
<211> 3129
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1555)..(1896)

<400> 40
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60

tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780

tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840

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aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960

tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260

cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500

actactctac tactataata ccccaaccca actcatattc aatactactc tact atg   1557
                                                          Met
                                                           1

gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg   1605
Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
               5                  10                  15

aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt   1653
Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
          20                  25                  30

gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc   1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
     35                  40                  45

ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt   1749
Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
 50                  55                  60                  65

gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg   1797
Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
                70                  75                  80

atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt   1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
               85                  90                  95

gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg   1893
Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
          100                 105                 110

gct taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg        1946
Ala

agagcatgga atattgtatc cgaccatgta acagtataat aactgagctc catctcactt 2006
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cttctatgaa taaacaaagg atgttatgat atattaacac tctatctatg caccttattg 2066

ttctatgata aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat 2126

gcttcaaata gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta 2186

gcattgtgaa cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt 2246

ctccatttat atattatata ttacccactt atgtattata ttaggatgtt aaggagacat 2306

aacaattata aagagagaag tttgtatcca tttatatatt atatactacc catttatata 2366

ttatacttat ccacttattt aatgtcttta taaggtttga tccatgatat ttctaatatt 2426

ttagttgata tgtatatgaa agggtactat ttgaactctc ttactctgta taaaggttgg 2486

atcatcctta aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat 2546

gagttggttt gataaaatat tgaaggattt aaaataataa taaataataa ataacatata 2606

atatatgtat ataaatttat tataatataa catttatcta taaaaaagta aatattgtca 2666

taaatctata caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa 2726

catatttgac tttttggtta tttaacaaat tattatttaa cactatatga aatttttttt 2786

ttttatcggc aaggaaataa aattaaatta ggagggacaa tggtgtgtcc caatccttat 2846

acaaccaact tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aagggaaatt 2906

ttttaatttg ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc 2966

cttttagcag tagagcaatg gttgaccgtg tgcttagctt cttttatttt attttttttat 3026

cagcaaagaa taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa 3086

accccaaaaa caagtttcct agcaccctac caactaaggt acc 3129

<210> 41
<211> 114
<212> PRT
<213> Arabidopsis thaliana

<400> 41

Met	Ala	Ser	Glu	Glu	Gly	Gln	Val	Ile	Ala	Cys	His	Thr	Val	Glu	Thr
1				5				10					15		
Trp	Asn	Glu	Gln	Leu	Gln	Lys	Ala	Asn	Glu	Ser	Lys	Thr	Leu	Val	Val
		20					25					30			
Val	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
	35					40					45				
Phe	Phe	Ala	Asp	Leu	Ala	Lys	Lys	Leu	Pro	Asn	Val	Leu	Phe	Leu	Lys
50					55					60					

Val Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln
65 70 75 80

Ala Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys
85 90 95

Val Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His
100 105 110

Leu Ala

<210> 42
<211> 3888
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1555)..(1908)

<220>
<221> CDS
<222> (2149)..(2655)

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin Trxh-phaseolin terminator

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ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780

tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840

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aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960

tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260

cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500

actactctac tactataata ccccaaccca actcatattc aatactactc tact atg   1557
                                                          Met
                                                           1

gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag   1605
Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
               5                  10                  15

tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga   1653
Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
          20                  25                  30

gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct   1701
Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
      35                  40                  45

gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt   1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val
  50                  55                  60                  65

gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc   1797
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe
                  70                  75                  80

agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc   1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr
              85                  90                  95

ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc   1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe
          100                 105                 110

tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa   1948
Ser Trp Ile Tyr Lys
     115
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tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa 2008

tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga 2068

cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat 2128

acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac 2181
                      Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp
                          120                 125

aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg   2229
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu
130                 135                 140                 145

aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat   2277
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His
                150                 155                 160

gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gct tcg gaa   2325
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu
            165                 170                 175

gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg aac gag cag   2373
Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln
        180                 185                 190

ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt gat ttc acg   2421
Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr
    195                 200                 205

gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc ttt gct gat   2469
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp
210                 215                 220                 225

ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt gat act gat   2517
Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp
                230                 235                 240

gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg atg cca acc   2565
Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr
            245                 250                 255

ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt gtt gga gcc   2613
Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala
        260                 265                 270

aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg gct           2655
Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu Ala
    275                 280                 285

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715

atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775

taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835

aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895
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gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955

cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015

atattatata ttacccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075

aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat 3135

ccacttattt aatgtcttta taaggtttga tccatgatat ttctaatatt ttagttgata 3195

tgtatatgaa agggtactat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255

aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt 3315

gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375

ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435

caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa catatttgac 3495

tttttggtta tttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc 3555

aaggaaataa aattaaatta ggagggacaa tggtgtgtcc caatccttat acaaccaact 3615

tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aagggaaatt ttttaatttg 3675

ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc cttttagcag 3735

tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat cagcaaagaa 3795

taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa 3855

caagtttcct agcaccctac caactaaggt acc 3888

<210> 43
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin Trxh-phaseolin terminator

<400> 43

Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly	Arg	Asp
1				5				10					15		

Gln	Tyr	Pro	Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met	Ser	Gly
		20					25					30			

Arg	Gly	Ser	Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala	Ala	Thr
		35					40					45			

Ala	Val	Thr	Ala	Gly	Gly	Ser	Leu	Leu	Val	Leu	Ser	Ser	Leu	Thr	Leu
	50					55					60				

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
100 105 110

Phe Ser Trp Ile Tyr Lys
115

<210> 44
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin Trxh-phaseolin terminator

<400> 44
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu Glu Gly Gln Val Ile
50 55 60

Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln Leu Gln Lys Ala Asn
65 70 75 80

Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr Ala Ser Trp Cys Gly
85 90 95

Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp Leu Ala Lys Lys Leu
100 105 110

Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp Glu Leu Lys Ser Val
115 120 125

Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr Phe Met Phe Leu Lys
130 135 140

Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala Lys Lys Asp Glu Leu
145 150 155 160

Gln Ser Thr Ile Ala Lys His Leu Ala
165

<210> 45
<211> 3888
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-Trxh oleosin-phaseolin terminator

<220>
<221> CDS
<222> (1555)..(2250)

<220>
<221> CDS
<222> (2491)..(2655)

<400> 45
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60

tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780

tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840

aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960

tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200

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catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260

cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500

actactctac tactataata ccccaaccca actcatattc aatactactc tact atg   1557
                                                           Met
                                                            1

gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg   1605
Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
                5                  10                  15

aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt   1653
Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
            20                  25                  30

gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc   1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
        35                  40                  45

ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt   1749
Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
    50                  55                  60                  65

gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg   1797
Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
                70                  75                  80

atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt   1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
            85                  90                  95

gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg   1893
Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
        100                 105                 110

gct atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga   1941
Ala Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg
    115                 120                 125

gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc   1989
Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser
130                 135                 140                 145

gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct gca   2037
Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala
                150                 155                 160

act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc   2085
Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr
            165                 170                 175
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ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt   2133
Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val
        180                 185                 190

atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc   2181
Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu
    195                 200                 205

atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc   2229
Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr
210                 215                 220                 225

gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa      2280
Val Phe Ser Trp Ile Tyr Lys
                230

ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc 2340

gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata 2400

cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc 2460

ttggtatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag   2514
                                Tyr Ala Thr Gly Glu His Pro Gln
                                    235                 240

gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct   2562
Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala
                245                 250                 255

cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt   2610
Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly
            260                 265                 270

ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act       2655
Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
        275                 280                 285

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715

atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775

taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835

aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895

gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955

cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015

atattatata ttacccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075

aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat 3135

ccacttattt aatgtcttta taaggtttga tccatgatat ttctaatatt ttagttgata 3195

tgtatatgaa agggtactat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255
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aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt 3315

gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375

ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435

caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa catatttgac 3495

tttttggtta tttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc 3555

aaggaaataa aattaaatta ggagggacaa tggtgtgtcc caatccttat acaaccaact 3615

tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aagggaaatt ttttaatttg 3675

ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc cttttagcag 3735

tagagcaatg gttgaccgtg tgcttagctt cttttatttt attttttttat cagcaaagaa 3795

taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa 3855

caagtttcct agcaccctac caactaaggt acc 3888

<210> 46
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-Trxh oleosin-phaseolin terminator

<400> 46

Met	Ala	Ser	Glu	Glu	Gly	Gln	Val	Ile	Ala	Cys	His	Thr	Val	Glu	Thr
1				5				10					15		
Trp	Asn	Glu	Gln	Leu	Gln	Lys	Ala	Asn	Glu	Ser	Lys	Thr	Leu	Val	Val
			20					25				30			
Val	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
		35					40					45			
Phe	Phe	Ala	Asp	Leu	Ala	Lys	Lys	Leu	Pro	Asn	Val	Leu	Phe	Leu	Lys
	50					55					60				
Val	Asp	Thr	Asp	Glu	Leu	Lys	Ser	Val	Ala	Ser	Asp	Trp	Ala	Ile	Gln
65					70					75					80
Ala	Met	Pro	Thr	Phe	Met	Phe	Leu	Lys	Glu	Gly	Lys	Ile	Leu	Asp	Lys
				85					90					95	
Val	Val	Gly	Ala	Lys	Lys	Asp	Glu	Leu	Gln	Ser	Thr	Ile	Ala	Lys	His
			100					105					110		
Leu	Ala	Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly
		115					120					125			

Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
130 135 140

Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala
145 150 155 160

Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu
165 170 175

Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu
180 185 190

Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu
195 200 205

Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile
210 215 220

Thr Val Phe Ser Trp Ile Tyr Lys
225 230

<210> 47
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-Trxh oleosin-phaseolin terminator

<400> 47
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr
50 55

<210> 48
<211> 3787
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-thioredoxin reductase-phaseolin terminator

<220>
<221> CDS
<222> (1555)..(2553)

<400> 48
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60

tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780

tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840

aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960

tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260

cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500

actactctac tactataata ccccaaccca actcatattc aatactactc tact atg 1557
Met
1

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aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc   1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly
                5                  10                  15

cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa   1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys
            20                  25                  30

cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt   1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly
        35                  40                  45

caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa   1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu
    50                  55                  60                  65

ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag   1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu
                70                  75                  80

cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc   1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe
            85                  90                  95

tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct   1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala
        100                 105                 110

gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc   1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe
    115                 120                 125

gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc   1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser
130                 135                 140                 145

gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct   2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro
                150                 155                 160

ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt   2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe
            165                 170                 175

ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct   2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala
        180                 185                 190

ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag   2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys
    195                 200                 205

att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga   2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly
210                 215                 220                 225
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gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga   2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly
                230                 235                 240

gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat   2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His
            245                 250                 255

gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat   2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp
        260                 265                 270

ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga   2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly
    275                 280                 285

gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc   2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile
290                 295                 300                 305

act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac   2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr
                310                 315                 320

tta caa gag att gga tct cag caa ggt aag agt gat tgaagcttaa        2563
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
            325                 330

taagtatgaa ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat 2623

ccgaccatgt aacagtataa taactgagct ccatctcact tcttctatga ataaacaaag 2683

gatgttatga tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc 2743

ttattattat aaatcatctg aatcgtgacg gcttatggaa tgcttcaaat agtacaaaaa 2803

caaatgtgta ctataagact ttctaaacaa ttctaacttt agcattgtga acgagacata 2863

agtgttaaga agacataaca attataatgg aagaagtttg tctccattta tatattatat 2923

attacccact tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa 2983

gtttgtatcc atttatatat tatatactac ccatttatat attatactta tccacttatt 3043

taatgtcttt ataaggtttg atccatgata tttctaatat tttagttgat atgtatatga 3103

aagggtacta tttgaactct cttactctgt ataaaggttg gatcatcctt aaagtgggtc 3163

tatttaattt tattgcttct tacagataaa aaaaaaatta tgagttggtt tgataaaata 3223

ttgaaggatt taaaataata ataaataata aataacatat aatatatgta tataaattta 3283

ttataatata acatttatct ataaaaaagt aaatattgtc ataaatctat acaatcgttt 3343

agccttgctg gacgactctc aattatttaa acgagagtaa acatatttga ctttttggtt 3403

atttaacaaa ttattattta acactatatg aaatttttt tttttatcgg caaggaaata 3463
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aaattaaatt aggagggaca atggtgtgtc ccaatcctta tacaaccaac ttccacagga 3523

aggtcaggtc ggggacaaca aaaaaacagg caagggaaat tttttaattt gggttgtctt 3583

gtttgctgca taatttatgc agtaaaacac tacacataac ccttttagca gtagagcaat 3643

ggttgaccgt gtgcttagct tcttttattt tatttttta tcagcaaaga ataaataaaa 3703

taaaatgaga cacttcaggg atgtttcaac ccttatacaa aaccccaaaa acaagtttcc 3763

tagcacccta ccaactaagg tacc 3787

<210> 49
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-thioredoxin reductase-phaseolin terminator

<400> 49

Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
1 5 10 15

Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
35 40 45

Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145 150 155 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 230 235 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
245 250 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
290 295 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305 310 315 320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
325 330

<210> 50
<211> 4546
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin thioredoxin reducatse-phaseolin terminator

<220>
<221> CDS
<222> (1555)..(1908)

<220>
<221> CDS
<222> (2149)..(3312)

<400> 50
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60

tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

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ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360
caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600
aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840
aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960
tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020
atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080
atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260
cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500
actactctac tactataata ccccaaccca actcatattc aatactactc tact atg    1557
                                                          Met
                                                            1

gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag    1605
Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
                5                  10                  15

tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga    1653
Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
            20                  25                  30

gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct    1701
Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
        35                  40                  45
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gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt   1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val
 50                  55                  60                  65

gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc   1797
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe
                 70                  75                  80

agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc   1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr
            85                  90                  95

ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc   1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe
        100                 105                 110

tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa   1948
Ser Trp Ile Tyr Lys
    115

tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa 2008

tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga 2068

cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat 2128

acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac 2181
                      Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp
                          120                 125

aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg   2229
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu
130                 135                 140                 145

aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat   2277
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His
                150                 155                 160

gac cgt gac cgt act cgt ggt ggc cag cac act acc atg aat ggt ctc   2325
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Asn Gly Leu
            165                 170                 175

gaa act cac aac aca agg ctc tgt atc gta gga agt ggc cca gcg gca   2373
Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly Pro Ala Ala
        180                 185                 190

cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa cct ctt ctc   2421
His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Leu Leu
    195                 200                 205

ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt caa cta aca   2469
Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly Gln Leu Thr
210                 215                 220                 225

acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa ggt att ctc   2517
Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu
                230                 235                 240
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gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag cga ttc ggt   2565
Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu Arg Phe Gly
            245                 250                 255

act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc tct tcg aaa   2613
Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe Ser Ser Lys
        260                 265                 270

ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct gac gct gtg   2661
Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala Asp Ala Val
    275                 280                 285

att ctc gct act gga gct gtg gct aag cgg ctt agc ttc gtt gga tct   2709
Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe Val Gly Ser
290                 295                 300                 305

ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc gct tgt gct   2757
Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala
                310                 315                 320

gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct ctt gcg gtg   2805
Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Leu Ala Val
            325                 330                 335

atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt ctt aca aaa   2853
Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys
        340                 345                 350

tat gga tct aaa gtg tat ata atc cat agg aga gat gct ttt aga gcg   2901
Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala Phe Arg Ala
    355                 360                 365

tct aag att atg cag cag cga gct ttg tct aat cct aag att gat gtg   2949
Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys Ile Asp Val
370                 375                 380                 385

att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga gaa aga gat   2997
Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp
                390                 395                 400

gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga gat gtt tct   3045
Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly Asp Val Ser
            405                 410                 415

gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat gag cca gct   3093
Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala
        420                 425                 430

acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat ggt tat gtt   3141
Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val
    435                 440                 445

gtc acg aag cct ggt act aca cag act agc gtt ccc gga gtt ttc gct   3189
Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala
450                 455                 460                 465
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gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc act gct gca   3237
Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala
                470                 475                 480

gga act ggg tgc atg gca gct ttg gat gca gag cat tac tta caa gag   3285
Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu
            485                 490                 495

att gga tct cag caa ggt aag agt gat tgaagcttaa taagtatgaa         3332
Ile Gly Ser Gln Gln Gly Lys Ser Asp
        500                 505

ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat ccgaccatgt 3392

aacagtataa taactgagct ccatctcact tcttctatga ataaacaaag gatgttatga 3452

tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc ttattattat 3512

aaatcatctg aatcgtgacg gcttatggaa tgcttcaaat agtacaaaaa caaatgtgta 3572

ctataagact ttctaaacaa ttctaacttt agcattgtga acgagacata agtgttaaga 3632

agacataaca attataatgg aagaagtttg tctccattta tatattatat attacccact 3692

tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa gtttgtatcc 3752

atttatatat tatatactac ccatttatat attatactta tccacttatt taatgtcttt 3812

ataaggtttg atccatgata tttctaatat tttagttgat atgtatatga aagggtacta 3872

tttgaactct cttactctgt ataaaggttg gatcatcctt aaagtgggtc tatttaattt 3932

tattgcttct tacagataaa aaaaaaatta tgagttggtt tgataaaata ttgaaggatt 3992

taaaataata ataaataata aataacatat aatatatgta tataaattta ttataatata 4052

acatttatct ataaaaaagt aaatattgtc ataaatctat acaatcgttt agccttgctg 4112

gacgactctc aattatttaa acgagagtaa acatatttga ctttttggtt atttaacaaa 4172

ttattattta acactatatg aaatttttt tttttatcgg caaggaaata aaattaaatt 4232

aggagggaca atggtgtgtc ccaatcctta tacaaccaac ttccacagga aggtcaggtc 4292

ggggacaaca aaaaaacagg caagggaaat tttttaattt gggttgtctt gtttgctgca 4352

taatttatgc agtaaaacac tacacataac ccttttagca gtagagcaat ggttgaccgt 4412

gtgcttagct tcttttattt tatttttta tcagcaaaga ataaataaaa taaaatgaga 4472

cacttcaggg atgtttcaac ccttatacaa aaccccaaaa acaagtttcc tagcacccta 4532

ccaactaagg tacc                                                   4546
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<210> 51
<211> 118

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin thioredoxin reducatse-phaseolin terminator

<400> 51
Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1 5 10 15

Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
20 25 30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
35 40 45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
50 55 60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
100 105 110

Phe Ser Trp Ile Tyr Lys
115

<210> 52
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-oleosin thioredoxin reducatse-phaseolin terminator

<400> 52
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Met Asn Gly Leu Glu Thr His Asn Thr
50 55 60

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Arg Leu Cys Ile Val Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile
 65                  70                  75                  80

Tyr Ala Ala Arg Ala Glu Leu Lys Pro Leu Leu Phe Glu Gly Trp Met
                 85                  90                  95

Ala Asn Asp Ile Ala Pro Gly Gly Gln Leu Thr Thr Thr Thr Asp Val
            100                 105                 110

Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu Gly Val Glu Leu Thr
        115                 120                 125

Asp Lys Phe Arg Lys Gln Ser Glu Arg Phe Gly Thr Thr Ile Phe Thr
    130                 135                 140

Glu Thr Val Thr Lys Val Asp Phe Ser Ser Lys Pro Phe Lys Leu Phe
145                 150                 155                 160

Thr Asp Ser Lys Ala Ile Leu Ala Asp Ala Val Ile Leu Ala Thr Gly
                165                 170                 175

Ala Val Ala Lys Arg Leu Ser Phe Val Gly Ser Gly Glu Gly Ser Gly
            180                 185                 190

Gly Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala
        195                 200                 205

Ala Pro Ile Phe Arg Asn Lys Pro Leu Ala Val Ile Gly Gly Gly Asp
    210                 215                 220

Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Lys Val
225                 230                 235                 240

Tyr Ile Ile His Arg Arg Asp Ala Phe Arg Ala Ser Lys Ile Met Gln
                245                 250                 255

Gln Arg Ala Leu Ser Asn Pro Lys Ile Asp Val Ile Trp Asn Ser Ser
            260                 265                 270

Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp Val Leu Gly Gly Leu
        275                 280                 285

Lys Val Lys Asn Val Val Thr Gly Asp Val Ser Asp Leu Lys Val Ser
    290                 295                 300

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Asp
305                 310                 315                 320

Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
                325                 330                 335

Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gln
            340                 345                 350

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Thr Gly Cys Met
        355                 360                 365
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Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ser Gln Gln
370 375 380

Gly Lys Ser Asp
385

<210> 53
<211> 4545
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-thioredoxin reductase oleosin-phaseolin terminator

<220>
<221> CDS
<222> (1555)..(2907)

<220>
<221> CDS
<222> (3148)..(3312)

<400> 53
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60

tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360

caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780

tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840

aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960

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tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260

cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500

actactctac tactataata ccccaaccca actcatattc aatactactc tact atg   1557
                                                          Met
                                                            1

aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc   1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly
                5                  10                  15

cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa   1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys
            20                  25                  30

cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt   1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly
        35                  40                  45

caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa   1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu
    50                  55                  60                  65

ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag   1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu
                70                  75                  80

cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc   1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe
            85                  90                  95

tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct   1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala
        100                 105                 110

gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc   1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe
    115                 120                 125

gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc   1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser
130                 135                 140                 145
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gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct   2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro
                150                 155                 160

ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt   2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe
            165                 170                 175

ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct   2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala
        180                 185                 190

ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag   2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys
    195                 200                 205

att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga   2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly
210                 215                 220                 225

gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga   2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly
                230                 235                 240

gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat   2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His
            245                 250                 255

gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat   2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp
        260                 265                 270

ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga   2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly
    275                 280                 285

gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc   2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile
290                 295                 300                 305

act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac   2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr
                310                 315                 320

tta caa gag att gga tct cag caa ggt aag agt gat atg gcg gat aca   2565
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp Thr
            325                 330                 335

gct aga gga acc cat cac gat atc atc ggc aga gac cag tac ccg atg   2613
Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met
        340                 345                 350

atg ggc cga gac cga gac cag tac cag atg tcc gga cga gga tct gac   2661
Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp
    355                 360                 365
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tac tcc aag tct agg cag att gct aaa gct gca act gct gtc aca gct   2709
Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala
370                 375                 380                 385

ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt gga act gtc   2757
Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val
                390                 395                 400

ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc agc cca atc   2805
Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile
            405                 410                 415

ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc ggt ttt ctt   2853
Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu
        420                 425                 430

tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc tct tgg att   2901
Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile
    435                 440                 445

tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa tatgtgcatg    2957
Tyr Lys
450

catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa tgtaacaata 3017

agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga cctagctagc 3077

ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat acctattgat 3137

tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac aag ttg    3186
          Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu
                  455                 460

gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg aaa gac   3234
Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp
465                 470                 475                 480

aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat gac cgt   3282
Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg
                485                 490                 495

gac cgt act cgt ggt ggc cag cac act act taagcttaat aagtatgaac     3332
Asp Arg Thr Arg Gly Gly Gln His Thr Thr
            500                 505

taaaatgcat gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta 3392

acagtataat aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat 3452

atattaacac tctatctatg caccttattg ttctatgata aatttcctct tattattata 3512

aatcatctga atcgtgacgg cttatggaat gcttcaaata gtacaaaaac aaatgtgtac 3572

tataagactt tctaaacaat tctaacttta gcattgtgaa cgagacataa gtgttaagaa 3632

gacataacaa ttataatgga agaagtttgt ctccatttat atattatata ttacccactt 3692
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atgtattata ttaggatgtt aaggagacat aacaattata aagagagaag tttgtatcca 3752

tttatatatt atatactacc catttatata ttatacttat ccacttattt aatgtcttta 3812

taaggtttga tccatgatat ttctaatatt ttagttgata tgtatatgaa agggtactat 3872

ttgaactctc ttactctgta taaaggttgg atcatcctta aagtgggtct atttaatttt 3932

attgcttctt acagataaaa aaaaaattat gagttggttt gataaaatat tgaaggattt 3992

aaaataataa taaataataa ataacatata atatatgtat ataaatttat tataatataa 4052

catttatcta taaaaaagta aatattgtca taaatctata caatcgttta gccttgctgg 4112

acgactctca attatttaaa cgagagtaaa catatttgac tttttggtta tttaacaaat 4172

tattatttaa cactatatga aatttttttt ttttatcggc aaggaaataa aattaaatta 4232

ggagggacaa tggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggtcg 4292

gggacaacaa aaaaacaggc aagggaaatt ttttaatttg ggttgtcttg tttgctgcat 4352

aatttatgca gtaaaacact acacataacc cttttagcag tagagcaatg gttgaccgtg 4412

tgcttagctt cttttatttt atttttttat cagcaaagaa taaataaaat aaaatgagac 4472

acttcaggga tgtttcaacc cttatacaaa accccaaaaa caagtttcct agcaccctac 4532

caactaaggt acc 4545

<210> 54
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-thioredoxin reductase oleosin-phaseolin terminator

<400> 54

Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser
1				5				10						15	
Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu
			20					25					30		
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly
		35					40					45			
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro
	50					55					60				
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser
65					70					75					80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145 150 155 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 230 235 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
245 250 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
290 295 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305 310 315 320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp
325 330 335

Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro
340 345 350

Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser
355 360 365

Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr
370 375 380

Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr
385 390 395 400

Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro
405 410 415

Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe
420 425 430

Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp
435 440 445

Ile Tyr Lys
450

<210> 55
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin promoter-thioredoxin reductase oleosin-phaseolin terminator

<400> 55
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr
50 55